STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 148568

TO: Nita M Minnifield
Location: 3c01 / 3c18
Monday, March 28, 2005
Art Unit: 1645
Phone: 571-272-0860
Serial Number: 09 / 970076

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-22504

jan.delaval@uspto.gov

Search Notes

From:	Chan, Christina
Sent:	Tuesday, March 22, 2005 4:42 PM
To:	Minnifield, Nita; STIC-Biotech/ChemLib
Subject:	RE: interference

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From:	Minnifield, Nita
Sent:	Tuesday, March 22, 2005 4:38 PM
To:	Chan, Christina
Subject:	interference

Christina, please approve, 2 month amdt.

STIC

09/970076

Please do an interference sequence search on SEQ ID NO: 2, 6, 8 and 10 of the above application.

Please search against aa and nt databases.

Please provide a paper copy of the results.

Thanks,
Minnifield

71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 25, 2005, 08:40:30 ; Search time 673.964 Seconds
(without alignments)
3253.936 Million cell updates/sec

Title: US-09-970-076-2
Perfect score: 1914
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1894	99.0	5540	10	US-09-918-715-231	Sequence 231, App
5	1894	99.0	5540	18	US-10-301-822-198	Sequence 198, App
6	1894	99.0	5540	18	US-10-474-794-176	Sequence 176, App
7	1894	99.0	5540	18	US-10-474-794-231	Sequence 231, App
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13	1661	86.8	1674	15	US-10-201-292-17	Sequence 17, Appl
14	1650	86.2	1650	15	US-10-038-307-13	Sequence 13, Appl
15	1650	86.2	1650	15	US-10-038-307-15	Sequence 15, Appl
16	1650	86.2	1650	15	US-10-201-292-13	Sequence 13, Appl
17	1650	86.2	1650	15	US-10-201-292-15	Sequence 15, Appl
18	1649	86.2	1056	15	US-10-038-307-23	Sequence 23, Appl
19	1649	86.2	1056	15	US-10-201-292-23	Sequence 23, Appl
20	1649	86.2	1713	15	US-10-038-307-19	Sequence 19, Appl
21	1649	86.2	1713	15	US-10-201-292-19	Sequence 19, Appl
22	1649	86.2	2272	10	US-09-796-753-11	Sequence 11, Appl
23	1649	86.2	2272	15	US-10-038-307-1	Sequence 1, Appli
24	1649	86.2	2272	15	US-10-201-292-1	Sequence 1, Appli
25	1649	86.2	2353	14	US-10-198-846-9957	Sequence 9957, Ap
26	1640	85.7	1650	15	US-10-038-307-9	Sequence 9, Appli
27	1640	85.7	1650	15	US-10-201-292-9	Sequence 9, Appli
28	1636	85.5	1008	15	US-10-038-307-25	Sequence 25, Appl
29	1636	85.5	1008	15	US-10-201-292-25	Sequence 25, Appl
30	1634.5	85.4	1047	15	US-10-038-307-21	Sequence 21, Appl
31	1634.5	85.4	1047	15	US-10-201-292-21	Sequence 21, Appl
32	1548	80.9	1608	15	US-10-201-292-35	Sequence 35, Appl
33	1520	79.4	2397	17	US-10-062-674-1757	Sequence 1757, Ap
34	1509	78.8	1623	15	US-10-038-307-11	Sequence 11, Appl
35	1509	78.8	1623	15	US-10-201-292-11	Sequence 11, Appl
36	1423	74.3	1534	12	US-10-201-292-33	Sequence 33, Appl
37	1392	72.7	1609	10	US-10-037-270-8	Sequence 8, Appli
38	1392	72.7	1609	17	US-10-117-722-8	Sequence 8, Appli
39	1392	72.7	1718	18	US-10-357-930-30300	Sequence 30300, A
40	1313	68.6	1464	15	US-10-201-292-31	Sequence 31, Appl
41	1193	62.3	1401	15	US-10-201-292-27	Sequence 27, Appl
42	1193	62.3	1401	15	US-10-201-292-29	Sequence 29, Appl
43	962.5	50.3	2234	17	US-10-104-047-669	Sequence 669, App
44	962.5	50.3	4081	16	US-10-368-087-9	Sequence 9, Appli
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ALIGNMENTS

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; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA

OM protein - nucleic search, using frame_plus_p2n model

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                Copyright  GenCore version 5.1.6
                         (c) 1993 - 2005 Compugen Ltd.

Run on:     March 25, 2005, 06:07:28 ; Search time 116.423 Seconds
                                          (without alignments)
                                      3063.887 Million cell updates/sec

Title:           US-09-970-076-10
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Searched:        1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters:      2405568

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Post-processing: Minimum Match 0%
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           6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Query Length	DB	ID	Description
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5	128.5	11.4	3519	1	US-08-485-618-45	Sequence 45, Appl
6	128.5	11.4	3519	1	US-08-362-652-45	Sequence 45, Appl
7	128.5	11.4	3519	1	US-08-605-672-45	Sequence 45, Appl
8	128.5	11.4	3519	2	US-08-482-293A-45	Sequence 45, Appl
9	128.5	11.4	3519	2	US-08-943-363-45	Sequence 45, Appl
10	128.5	11.4	3519	3	US-09-193-043-45	Sequence 45, Appl
11	128.5	11.4	3519	3	US-09-688-307A-45	Sequence 45, Appl
12	128.5	11.4	3519	4	US-09-350-259-45	Sequence 45, Appl
13	128.5	11.4	3803	1	US-08-485-618-52	Sequence 52, Appl
14	128.5	11.4	3803	1	US-08-362-652-52	Sequence 52, Appl
15	128.5	11.4	3803	1	US-08-605-672-52	Sequence 52, Appl
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26	122	10.8	3528	2	US-08-943-363-36	Sequence 36, Appl
27	122	10.8	3528	3	US-09-193-043-36	Sequence 36, Appl
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ALIGNMENTS

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; Patent No. 6569662
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Liu, Chenghua
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Zhang, Jie
;   APPLICANT: Ren, Feiyan
;   APPLICANT: Chen, Rui-hong
;   APPLICANT: Zhao, Qing A.
;   APPLICANT: Wehrman, Tom
;   APPLICANT: Xue, Aidong J.
;   APPLICANT: Yang, Yonghong
;   APPLICANT: Wang, Jian-Rui
;   APPLICANT: Zhou, Ping
;   APPLICANT: Ma, Yunqing
;   APPLICANT: Wang, Dunrui
;   APPLICANT: Wang, Zhiwei
;   APPLICANT: John Tillinghast
;   APPLICANT: Drmanac, Radoje T.
;   TITLE OF INVENTION: 6569962el Nucleic Acids and
;   TITLE OF INVENTION: Polypeptides
;   FILE REFERENCE: 784CIP2B
;   CURRENT APPLICATION NUMBER: US/09/620,312D
;   CURRENT FILING DATE: 2000-07-19
;   PRIOR APPLICATION NUMBER: 09/552,317
;   PRIOR FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: 09/488,725
;   PRIOR FILING DATE: 2000-01-21
;   NUMBER OF SEQ ID NOS: 1105
;   SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 8
;   LENGTH: 1609
;   TYPE: DNA
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OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: March 25, 2005, 08:40:30 ; Search time 399.25 Seconds
(without alignments)
3253.936 Million cell updates/sec

Title: US-09-970-076-10
Perfect score: 1131
Sequence: 1 MSFIVFSTRGTTLMKLTEDR.........STSGFKEGNSHPCLPARPHT 218

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1131	100.0	1609	17	US-10-117-722-8	Sequence 8, Appli
3	1131	100.0	1718	18	US-10-357-930-30300	Sequence 30300, A
4	977	86.4	1534	15	US-10-201-292-33	Sequence 33, Appl
5	966.5	85.5	1608	15	US-10-201-292-35	Sequence 35, Appl
6	966	85.4	1008	15	US-10-038-307-25	Sequence 25, Appl
7	966	85.4	1008	15	US-10-201-292-25	Sequence 25, Appl
8	966	85.4	1047	15	US-10-038-307-21	Sequence 21, Appl
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11	966	85.4	1056	15	US-10-201-292-23	Sequence 23, Appl
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19	966	85.4	1650	15	US-10-201-292-9	Sequence 9, Appli
20	966	85.4	1650	15	US-10-201-292-13	Sequence 13, Appl
21	966	85.4	1650	15	US-10-201-292-15	Sequence 15, Appl
22	966	85.4	1674	15	US-10-038-307-17	Sequence 17, Appl
23	966	85.4	1674	15	US-10-201-292-17	Sequence 17, Appl
24	966	85.4	1713	15	US-10-038-307-19	Sequence 19, Appl
25	966	85.4	1713	15	US-10-201-292-19	Sequence 19, Appl
26	966	85.4	2272	10	US-09-796-753-11	Sequence 11, Appl
27	966	85.4	2272	15	US-10-038-307-1	Sequence 1, Appli
28	966	85.4	2272	15	US-10-201-292-1	Sequence 1, Appli
29	966	85.4	2353	14	US-10-198-846-9957	Sequence 9957, Ap
30	966	85.4	5540	10	US-09-918-715-176	Sequence 176, App
31	966	85.4	5540	10	US-09-918-715-231	Sequence 231, App
32	966	85.4	5540	15	US-10-301-822-198	Sequence 198, App
33	966	85.4	5540	18	US-10-474-794-176	Sequence 176, App
34	966	85.4	5540	18	US-10-474-794-231	Sequence 231, App
35	960	84.9	5220	10	US-09-918-715-186	Sequence 186, App
36	960	84.9	5220	10	US-09-918-715-300	Sequence 300, App
37	960	84.9	5220	18	US-10-474-794-186	Sequence 186, App
38	960	84.9	5220	18	US-10-474-794-300	Sequence 300, App
39	938	82.9	2397	17	US-10-062-674-1757	Sequence 1757, Ap
40	878	77.6	1464	15	US-10-201-292-31	Sequence 31, Appl
41	767	67.8	1401	15	US-10-201-292-27	Sequence 27, Appl
42	767	67.8	1401	15	US-10-201-292-29	Sequence 29, Appl
43	704	62.2	1650	13	US-10-047-542-98	Sequence 98, Appl
44	704	62.2	6602	13	US-10-047-542-100	Sequence 100, App
45	571	50.5	454	17	US-10-062-674-417	Sequence 417, App

ALIGNMENTS

RESULT 1
US-10-037-270-8
; Sequence 8, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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          GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:    March 23, 2005, 11:30:49 ; Search time 13.6709 Seconds
                                       (without alignments)
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Title:          US-09-970-076-10
Perfect score:  1131
Sequence:       1 MSFIVFSTRGTTLMKLTEDR.........STSGFKEGNSHPCLPARPHT 218

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       513545 seqs, 74649064 residues
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Total number of hits satisfying chosen parameters:　　　513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	128.5	11.4	1155	1	US-08-362-652-46	Sequence 46, Appl
4	128.5	11.4	1155	2	US-08-605-672-46	Sequence 46, Appl
5	128.5	11.4	1155	2	US-08-482-293A-46	Sequence 46, Appl
6	128.5	11.4	1155	3	US-08-943-363-46	Sequence 46, Appl
7	128.5	11.4	1155	3	US-09-193-043-46	Sequence 46, Appl
8	128.5	11.4	1155	4	US-09-688-307A-46	Sequence 46, Appl
9	128.5	11.4	1155	4	US-09-350-259-46	Sequence 46, Appl
10	128.5	11.4	1161	1	US-08-485-618-53	Sequence 53, Appl
11	128.5	11.4	1161	2	US-08-362-652-53	Sequence 53, Appl
12	128.5	11.4	1161	2	US-08-605-672-53	Sequence 53, Appl
13	128.5	11.4	1161	2	US-08-482-293A-53	Sequence 53, Appl
14	128.5	11.4	1161	3	US-08-943-363-53	Sequence 53, Appl
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16	128.5	11.4	1161	4	US-09-688-307A-53	Sequence 53, Appl
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18	122	10.8	1151	1	US-08-286-889-37	Sequence 37, Appl
19	122	10.8	1151	1	US-08-485-618-37	Sequence 37, Appl
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21	122	10.8	1151	2	US-08-605-672-37	Sequence 37, Appl
22	122	10.8	1151	2	US-08-482-293A-37	Sequence 37, Appl
23	122	10.8	1151	3	US-08-943-363-37	Sequence 37, Appl
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25	122	10.8	1151	4	US-09-688-307A-37	Sequence 37, Appl
26	122	10.8	1151	4	US-09-350-259-37	Sequence 37, Appl
27	122	10.8	1161	1	US-08-485-618-55	Sequence 55, Appl
28	122	10.8	1161	1	US-08-362-652-55	Sequence 55, Appl
29	122	10.8	1161	2	US-08-605-672-55	Sequence 55, Appl
30	122	10.8	1161	2	US-08-482-293A-55	Sequence 55, Appl
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33	122	10.8	1161	4	US-09-688-307A-55	Sequence 55, Appl
34	122	10.8	1161	4	US-09-350-259-55	Sequence 55, Appl
35	122	10.1	1161	1	US-08-173-497-2	Sequence 2, Appli
36	114	10.1	1161	1	US-08-286-889-2	Sequence 2, Appli
37	114	10.1	1161	1	US-08-485-618-2	Sequence 2, Appli
38	114	10.1	1161	1	US-08-485-618-99	Sequence 99, Appl
39	114	10.1	1161	1	US-08-362-652-2	Sequence 2, Appli
40	114	10.1	1161	2	US-08-605-672-2	Sequence 2, Appli
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ALIGNMENTS

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; Sequence 46, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
;  APPLICANT: Gallatin, W. Mich
;  APPLICANT: Van der Vieren, Monica
;  TITLE OF INVENTION:  No. 5470953e1 Human  2 Integrin Alpha Subunit
;  NUMBER OF SEQUENCES:  51
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 233 South Wacker Drive, 6300 Sear Tower
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: United States
;   ZIP: 60606-6402
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/286,889
;   FILING DATE:
;   CLASSIFICATION:  435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/173,497
;   FILING DATE:  23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Williams Jr., Joseph A.
;   REGISTRATION NUMBER:  P38,659
;   REFERENCE/DOCKET NUMBER:  27866/32168
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-474-6300
;   TELEFAX: 312-474-0448
;   TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 1155 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-286-889-46

Query Match             11.4%;  Score 128.5; DB 1; Length 1155;
Best Local Similarity   28.9%;  Pred. No. 1.6e-05;
Matches  50;  Conservative 31; Mismatches 69; Indels 23; Gaps 9;

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                 GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          March 23, 2005, 11:43:59 ; Search time 39.9838 Seconds
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Perfect score:   1131
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Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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8	966	85.4	342	14	US-10-201-292-22	Sequence 22, Appl
9	966	85.4	345	14	US-10-038-307-24	Sequence 24, Appl
10	966	85.4	345	14	US-10-201-292-24	Sequence 24, Appl
11	966	85.4	403	11	US-09-833-245-621	Sequence 621, App
12	966	85.4	529	14	US-10-201-292-36	Sequence 36, Appl
13	966	85.4	551	14	US-10-038-307-18	Sequence 18, Appl
14	966	85.4	551	14	US-10-201-292-18	Sequence 18, Appl
15	966	85.4	564	10	US-09-918-715-187	Sequence 187, App
16	966	85.4	564	10	US-09-918-715-232	Sequence 232, App
17	966	85.4	564	14	US-10-038-307-20	Sequence 20, Appl
18	966	85.4	564	14	US-10-201-292-20	Sequence 20, Appl
19	966	85.4	564	16	US-10-301-822-199	Sequence 199, App
20	966	85.0	564	16	US-10-408-765A-1823	Sequence 1823, Ap
21	961	85.0	403	11	US-09-833-245-620	Sequence 620, App
22	960	84.9	562	10	US-09-918-715-194	Sequence 194, App
23	960	84.9	562	10	US-09-918-715-301	Sequence 301, App
24	945	83.6	534	14	US-10-038-307-12	Sequence 12, Appl
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28	945	83.6	543	14	US-10-038-307-16	Sequence 16, Appl
29	945	83.6	543	14	US-10-201-292-10	Sequence 10, Appl
30	945	83.6	543	14	US-10-201-292-14	Sequence 14, Appl
31	945	83.6	543	14	US-10-201-292-16	Sequence 16, Appl
32	877	77.5	543	14	US-10-201-292-28	Sequence 28, Appl
33	767	67.8	479	14	US-10-201-292-30	Sequence 30, Appl
34	757	66.9	460	14	US-10-201-292-32	Sequence 32, Appl
35	704	62.2	460	14	US-10-047-542-99	Sequence 99, Appl
36	538	47.6	245	13	US-10-094-749-2134	Sequence 2134, Ap
37	506	44.7	272	15	US-10-264-237-1574	Sequence 1574, Ap
38	506	44.7	488	10	US-09-796-753-52	Sequence 52, Appl
39	506	44.7	488	14	US-10-038-307-6	Sequence 6, Appli
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ALIGNMENTS

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; Sequence 34, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
;   APPLICANT:  James B. ROTTMAN
;   APPLICANT:  Theresa L. O'KEEFE
;   APPLICANT:  Engin OZKAYNAK
;   APPLICANT:  Judith J. HEALEY
;   TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
;   FILE REFERENCE: 7853-253-999
;   CURRENT APPLICATION NUMBER: US/10/201,292
;   CURRENT FILING DATE:  2003-02-14
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 34
;   LENGTH: 504
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-201-292-34

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Matches  194;  Conservative   9;  Mismatches   3;  Indels   7;  Gaps   1;

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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  140 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 199

Qy  121 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVRGNGFRHARNVDRVLCSF 180
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                    GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:      March 25, 2005, 06:07:28 ; Search time 177.84 Seconds
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                                    3063.887 Million cell updates/sec

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Searched:      1202784 seqs, 818138359 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	166	9.6	3519	1	US-08-485-618-45	Sequence 45, Appl
6	166	9.6	3519	1	US-08-362-652-45	Sequence 45, Appl
7	166	9.6	3519	1	US-08-605-672-45	Sequence 45, Appl
8	166	9.6	3519	2	US-08-482-293A-45	Sequence 45, Appl
9	166	9.6	3519	2	US-08-943-363-45	Sequence 45, Appl
10	166	9.6	3519	3	US-09-193-043-45	Sequence 45, Appl
11	166	9.6	3519	3	US-09-688-307A-45	Sequence 45, Appl
12	166	9.6	3519	4	US-09-350-259-45	Sequence 45, Appl
13	166	9.6	3803	1	US-08-485-618-52	Sequence 52, Appl
14	166	9.6	3803	1	US-08-362-652-52	Sequence 52, Appl
15	166	9.6	3803	2	US-08-605-672-52	Sequence 52, Appl
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17	166	9.6	3803	3	US-08-943-363-52	Sequence 52, Appl
18	166	9.6	3803	3	US-09-193-043-52	Sequence 52, Appl
19	166	9.6	3803	4	US-09-688-307A-52	Sequence 52, Appl
20	166	9.6	3803	4	US-09-350-259-52	Sequence 52, Appl
21	159.5	9.2	2499	1	US-08-485-618-96	Sequence 96, Appl
22	159.5	9.2	2499	1	US-08-605-672-96	Sequence 96, Appl
23	159.5	9.2	2499	2	US-08-482-293A-96	Sequence 96, Appl
24	159.5	9.2	2499	2	US-08-943-363-96	Sequence 96, Appl
25	159.5	9.2	2499	3	US-09-193-043-96	Sequence 96, Appl
26	159.5	9.2	2499	3	US-09-688-307A-96	Sequence 96, Appl
27	159.5	9.2	2499	4	US-09-350-259-96	Sequence 96, Appl
28	159.5	9.2	3528	1	US-08-286-889-36	Sequence 36, Appl
29	159.5	9.2	3528	1	US-08-485-618-36	Sequence 36, Appl
30	159.5	9.2	3528	1	US-08-362-652-36	Sequence 36, Appl
31	159.5	9.2	3528	1	US-08-605-672-36	Sequence 36, Appl
32	159.5	9.2	3528	2	US-08-482-293A-36	Sequence 36, Appl
33	159.5	9.2	3528	2	US-08-943-363-36	Sequence 36, Appl
34	159.5	9.2	3528	3	US-09-193-043-36	Sequence 36, Appl
35	159.5	9.2	3528	3	US-09-688-307A-36	Sequence 36, Appl
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41	159.5	9.2	3597	2	US-08-943-363-54	Sequence 54, Appl
42	159.5	9.2	3597	3	US-09-193-043-54	Sequence 54, Appl
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                            ALIGNMENTS

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; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y., Tom
;  APPLICANT: Liu, Chenghua
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Zhang, Jie
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Chen, Rui-hong
;  APPLICANT: Zhao, Qing A.
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: Yang, Yonghong
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Zhou, Ping
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Wang, Zhiwei
;  APPLICANT: John Tillinghast
;  APPLICANT: Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6569662el Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312D
;  CURRENT FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 1105
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 8
;  LENGTH: 1609
;  TYPE: DNA
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: March 25, 2005, 08:40:30 ; Search time 609.864 Seconds
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3253.936 Million cell updates/sec

Title: US-09-970-076-8
Perfect score: 1728
Sequence: 1 MATAERRALGIGFQWLSLAT.........TTHCSLHKIASGPTTAACME 333

Scoring table: BLOSUM62
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Searched: 5552208 seqs, 2979665951 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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3	1728	100.0	2272	15	US-09-796-753-11	Sequence 11, Appl
4	1728	100.0	2272	15	US-10-038-307-1	Sequence 1, Appli
5	1728	100.0	2353	14	US-10-201-292-1	Sequence 1, Appli
6	1728	100.0		15	US-10-198-846-9957	Sequence 9957, Ap
7	1718	99.4	1056	15	US-10-038-307-23	Sequence 23, Appl
8	1718	99.4	1056	15	US-10-201-292-23	Sequence 23, Appl
9	1713.5	99.2	1047	15	US-10-038-307-21	Sequence 21, Appl
10	1713.5	99.2	1047	15	US-10-201-292-21	Sequence 21, Appl
11	1650.5	95.5	1674	15	US-10-038-307-17	Sequence 17, Appl
12	1650.5	95.5	1674	15	US-10-201-292-17	Sequence 17, Appl
13	1649	95.4	1454	17	US-10-133-937-58	Sequence 58, Appl
14	1649	95.4	1454	17	US-10-159-563-58	Sequence 58, Appl
15	1649	95.4	1650	15	US-10-038-307-13	Sequence 13, Appl
16	1649	95.4	1650	15	US-10-038-307-15	Sequence 15, Appl
17	1649	95.4	1650	15	US-10-201-292-13	Sequence 13, Appl
18	1649	95.4	1650	15	US-10-201-292-15	Sequence 15, Appl
19	1649	95.4	5540	10	US-09-918-715-176	Sequence 176, App
20	1649	95.4	5540	10	US-09-918-715-231	Sequence 231, App
21	1649	95.4	5540	15	US-10-301-822-198	Sequence 198, App
22	1649	95.4	5540	18	US-10-474-794-176	Sequence 176, App
23	1649	95.4	5540	18	US-10-474-794-231	Sequence 231, App
24	1639	94.8	1650	15	US-10-038-307-9	Sequence 9, Appli
25	1639	94.8	1650	15	US-10-201-292-9	Sequence 9, Appli
26	1636	94.7	1008	15	US-10-038-307-25	Sequence 25, Appl
27	1636	94.7	1008	15	US-10-201-292-25	Sequence 25, Appl
28	1599	92.5	2397	17	US-10-062-674-1757	Sequence 1757, Ap
29	1556	90.0	1608	15	US-10-201-292-35	Sequence 35, Appl
30	1553	89.9	5220	10	US-09-918-715-300	Sequence 300, App
31	1553	89.9	5220	10	US-10-474-794-186	Sequence 186, App
32	1553	89.9	5220	18	US-10-474-794-300	Sequence 300, App
33	1508	87.3	1623	15	US-10-038-307-11	Sequence 11, Appl
34	1508	87.3	1623	15	US-10-201-292-11	Sequence 11, Appl
35	1423	82.3	1534	15	US-10-201-292-33	Sequence 33, Appl
36	1392	80.6	1609	15	US-10-037-270-8	Sequence 8, Appli
37	1392	80.6	1609	17	US-10-117-722-8	Sequence 8, Appli
38	1392	80.6	1718	18	US-10-357-930-30300	Sequence 30300, A
39	1313	76.0	1464	15	US-10-201-292-31	Sequence 31, Appl
40	1193	69.0	1401	15	US-10-201-292-27	Sequence 27, Appl
41	1193	69.0	1401	15	US-10-201-292-29	Sequence 29, Appl
42	903	52.3	1650	13	US-10-047-542-98	Sequence 98, App
43	903	52.3	6602	13	US-10-047-542-100	Sequence 100, App
44	800.5	46.3	2234	17	US-10-104-047-669	Sequence 669, App

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
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; Sequence 19, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-19

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                    GenCore version 5.1.6
               Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on:        March 23, 2005, 11:30:49 ; Search time 20.8827 Seconds
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Title:         US-09-970-076-8
Perfect score: 1728
Sequence:      1 MATAERRALGIGFQWLSLAT........THCSLHKIASGPTTAACME 333

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters:        513545

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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4	166	9.6	1155	2	US-08-605-672-46	Sequence 46, Appl
5	166	9.6	1155	2	US-08-482-293A-46	Sequence 46, Appl
6	166	9.6	1155	3	US-08-943-363-46	Sequence 46, Appl
7	166	9.6	1155	4	US-09-193-043-46	Sequence 46, Appl
8	166	9.6	1155	4	US-09-688-307A-46	Sequence 46, Appl
9	166	9.6	1155	4	US-09-350-259-46	Sequence 46, Appl
10	166	9.6	1161	1	US-08-485-618-53	Sequence 53, Appl
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12	166	9.6	1161	2	US-08-605-672-53	Sequence 53, Appl
13	166	9.6	1161	2	US-08-482-293A-53	Sequence 53, Appl
14	166	9.6	1161	2	US-08-943-363-53	Sequence 53, Appl
15	166	9.6	1161	3	US-09-193-043-53	Sequence 53, Appl
16	166	9.6	1161	4	US-09-688-307A-53	Sequence 53, Appl
17	166	9.6	1161	4	US-09-350-259-53	Sequence 53, Appl
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19	159.5	9.2	1151	1	US-08-485-618-37	Sequence 37, Appl
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21	159.5	9.2	1151	2	US-08-605-672-37	Sequence 37, Appl
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23	159.5	9.2	1151	2	US-08-943-363-37	Sequence 37, Appl
24	159.5	9.2	1151	3	US-09-193-043-37	Sequence 37, Appl
25	159.5	9.2	1151	4	US-09-688-307A-37	Sequence 37, Appl
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28	159.5	9.2	1161	1	US-08-286-889-2	Sequence 2, Appli
29	159.5	9.2	1161	1	US-08-485-618-2	Sequence 2, Appli
30	159.5	9.2	1161	1	US-08-485-618-55	Sequence 55, Appl
31	159.5	9.2	1161	1	US-08-485-618-99	Sequence 99, Appl
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33	159.5	9.2	1161	2	US-08-362-652-55	Sequence 55, Appl
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35	159.5	9.2	1161	2	US-08-605-672-55	Sequence 55, Appl
36	159.5	9.2	1161	2	US-08-605-672-99	Sequence 99, Appl
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38	159.5	9.2	1161	2	US-08-482-293A-55	Sequence 55, Appl
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41	159.5	9.2	1161	2	US-08-943-363-55	Sequence 55, Appl
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ALIGNMENTS

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; Patent No. 5470953
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; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human  2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-889-46

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        Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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8	1713.5	99.2	342	14	US-10-038-307-22	Sequence 22, Appl
9	1713.5	99.2	342	14	US-10-201-292-22	Sequence 22, Appl
10	1650.5	95.5	551	14	US-10-038-307-18	Sequence 18, Appl
11	1650.5	95.5	551	14	US-10-201-292-18	Sequence 18, Appl
12	1649	95.4	403	11	US-09-833-245-621	Sequence 621, App
13	1649	95.4	564	10	US-09-918-715-187	Sequence 187, App
14	1649	95.4	564	10	US-09-918-715-232	Sequence 232, App
15	1649	95.4	564	14	US-10-301-822-199	Sequence 199, App
16	1649	95.4	564	16	US-10-408-765A-1823	Sequence 1823, Ap
17	1644	95.1	403	14	US-09-833-245-620	Sequence 620, App
18	1636	94.7	328	14	US-10-038-307-26	Sequence 26, Appl
19	1636	94.7	328	14	US-10-201-292-26	Sequence 26, Appl
20	1628	94.2	543	14	US-10-038-307-16	Sequence 16, Appl
21	1628	94.2	543	14	US-10-038-307-14	Sequence 14, Appl
22	1628	94.2	543	14	US-10-201-292-14	Sequence 14, Appl
23	1628	94.2	543	14	US-10-201-292-16	Sequence 16, Appl
24	1618	93.6	543	14	US-10-038-307-10	Sequence 10, Appl
25	1618	93.6	543	14	US-10-201-292-10	Sequence 10, Appl
26	1556	90.0	529	14	US-10-201-292-36	Sequence 36, Appl
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28	1553	89.9	562	10	US-09-918-715-301	Sequence 301, App
29	1487	86.1	534	14	US-10-038-307-12	Sequence 12, Appl
30	1487	86.1	534	14	US-10-201-292-12	Sequence 12, Appl
31	1434.5	83.0	504	14	US-10-201-292-34	Sequence 34, Appl
32	1307	75.6	479	14	US-10-201-292-32	Sequence 32, Appl
33	1193	69.0	460	14	US-10-201-292-28	Sequence 28, Appl
34	1183	68.5	460	14	US-10-201-292-30	Sequence 30, Appl
35	903	52.3	538	13	US-10-047-542-99	Sequence 99, Appl
36	800.5	46.3	488	10	US-09-796-753-52	Sequence 52, Appl
37	800.5	46.3	488	14	US-10-038-307-6	Sequence 6, Appli
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39	800.5	46.3	488	14	US-10-368-087-16	Sequence 16, Appl
40	800.5	45.5	488	9	US-10-104-047-2639	Sequence 2639, Ap
41	785.5	45.5	587	9	US-09-764-870-312	Sequence 312, App
42	785.5	45.5	587	11	US-09-764-875-968	Sequence 968, App
43	785.5	45.5	587	14	US-10-125-540-312	Sequence 312, App
44	771	44.6	487	14	US-09-796-753-54	Sequence 54, Appl
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ALIGNMENTS

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; Sequence 12, Application US/0796753
; Publication No. US2003002799BA1
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;  APPLICANT:  McCarthy, Sean A.
;  TITLE OF INVENTION:  SECRETED PROTEINS AND USES THEREOF
;  FILE REFERENCE:  7853-227-999
;  CURRENT APPLICATION NUMBER:  US/09/796,753
;  CURRENT FILING DATE:  2001-03-01
;  PRIOR APPLICATION NUMBER:  09/183,175
;  PRIOR FILING DATE:  1998-10-30
;  PRIOR APPLICATION NUMBER:  09/223,094
;  PRIOR FILING DATE:  1998-12-30
;  PRIOR APPLICATION NUMBER:  09/223,546
;  PRIOR FILING DATE:  1998-12-30
;  PRIOR APPLICATION NUMBER:  09/224,246
;  PRIOR FILING DATE:  1998-12-30
;  PRIOR APPLICATION NUMBER:  09/259,388
;  PRIOR FILING DATE:  1999-02-26
;  PRIOR APPLICATION NUMBER:  60/122,458
;  PRIOR FILING DATE:  1999-03-01
;  PRIOR APPLICATION NUMBER:  09/312,359
;  PRIOR FILING DATE:  1999-05-14
;  PRIOR APPLICATION NUMBER:  09/336,536
;  PRIOR FILING DATE:  1999-06-18
;  PRIOR APPLICATION NUMBER:  09/342,687
;  PRIOR FILING DATE:  1999-06-29
;  PRIOR APPLICATION NUMBER:  09/345,464
;  PRIOR FILING DATE:  1999-06-30
;  PRIOR APPLICATION NUMBER:  09/365,164
;  PRIOR FILING DATE:  1999-07-30
;  PRIOR APPLICATION NUMBER:  09/399,723
;  PRIOR FILING DATE:  1999-09-20
;  PRIOR APPLICATION NUMBER:  09/409,634
;  PRIOR FILING DATE:  1999-09-30
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               GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:   March 25, 2005, 06:07:28 ; Search time 301.206 Seconds
                                      (without alignments)
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Searched:       1202784 seqs, 818133359 residues

Total number of hits satisfying chosen parameters:        2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1392	46.0	1609	4	US-09-620-312D-8	Sequence 8, Appli
3	1306	43.2	4210	4	US-09-774-528-297	Sequence 297, App
c 4	213	7.0	318	3	US-09-165-264-12	Sequence 12, Appl
c 5	213	7.0	320	3	US-09-165-264-14	Sequence 14, Appl
6	208.5	6.9	34230	4	US-09-949-016-12052	Sequence 12052, A
7	208.5	6.9	128470	4	US-09-949-016-13765	Sequence 13765, A
c 8	208	6.9	320	3	US-09-165-264-13	Sequence 13, Appl
9	207.5	6.9	865	4	US-09-270-767-11042	Sequence 11042, A
c 10	207.5	6.9	152132	4	US-09-949-016-13845	Sequence 13845, A
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13	205.5	6.8	51259	3	US-08-781-891-209	Sequence 209, App
14	205.5	6.8	51259	3	US-09-618-166-209	Sequence 209, App
c 15	205	6.8	320	3	US-09-165-264-11	Sequence 11, Appl
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c 17	205	6.8	936	4	US-09-270-767-19746	Sequence 19746, A
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19	203	6.7	319	3	US-09-165-264-8	Sequence 8, Appli
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22	200.5	6.6	1497	4	US-09-949-016-1237	Sequence 1237, Ap
23	200.5	6.6	12695	4	US-09-949-016-16775	Sequence 16775, A
24	199.5	6.6	324	3	US-09-547-693-234	Sequence 234, App
25	199	6.6	53577	3	US-08-658-136-1	Sequence 1, Appli
26	197.5	6.5	22431	4	US-09-949-016-14099	Sequence 14099, A
27	196.5	6.5	15252	4	US-09-949-016-13584	Sequence 13584, A
c 28	196.5	6.5	97195	4	US-09-949-016-12212	Sequence 12212, A
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32	195	6.4	16442	4	US-09-618-166-208	Sequence 208, App
33	194	6.4	53526	3	US-09-658-136-2	Sequence 2, Appli
34	193	6.4	11766	4	US-09-949-016-12531	Sequence 12531, A
c 35	193	6.4	11770	4	US-09-949-016-12720	Sequence 12720, A
c 36	193	6.4	11770	4	US-09-949-016-13487	Sequence 13487, A
c 37	193	6.4	11770	4	US-09-949-016-13488	Sequence 13488, A
c 38	192	6.3	43280	2	US-08-804-227C-1	Sequence 1, Appli
39	191.5	6.3	2230	1	US-08-217-327-5	Sequence 5, Appli
40	191.5	6.3	16782	4	US-09-949-016-17291	Sequence 17291, A
c 41	191.5	6.3	39154	4	US-09-949-016-12384	Sequence 12384, A
c 42	191.5	6.3	39154	4	US-09-949-016-12801	Sequence 12801, A
c 43	191.5	6.3	39443	4	US-09-949-016-14326	Sequence 14326, A
c 44	191.5	6.3	39443	4	US-09-949-016-14327	Sequence 14327, A
c 45	191.5	6.3	767677	4	US-09-949-016-12147	Sequence 12147, A

ALIGNMENTS

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; Sequence 250, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y., Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 678396 9el Nucleic Acids and
; TITLE OF INVENTION:   Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 250
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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11	2017	66.7	4417	15	US-09-796-753-23	Sequence 23, Appl
12	2017	66.7	4417	15	US-10-038-307-3	Sequence 3, Appli
13	2017	66.7	4417	15	US-10-201-292-3	Sequence 3, Appli
14	1894	62.6	1454	17	US-10-133-937-58	Sequence 58, Appl
15	1894	62.6	1454	17	US-10-159-563-58	Sequence 58, Appl
16	1661	54.9	1674	15	US-10-038-307-17	Sequence 17, Appl
17	1661	54.9	1674	15	US-10-201-292-17	Sequence 17, Appl
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33	1636	54.1	1008	15	US-10-201-292-25	Sequence 25, Appl
34	1634.5	54.0	1047	15	US-10-038-307-21	Sequence 21, Appl
35	1634.5	54.0	1047	15	US-10-201-292-21	Sequence 21, Appl
36	1557.5	51.5	1608	15	US-10-201-292-35	Sequence 35, Appl
37	1530	50.6	2397	17	US-10-062-674-1757	Sequence 1757, Ap
38	1509.5	49.9	1623	15	US-10-038-307-11	Sequence 11, Appl
39	1509.5	49.9	1623	15	US-10-201-292-11	Sequence 11, Appl
40	1423	47.0	1534	15	US-10-201-292-33	Sequence 33, Appl
41	1416.5	46.8	2234	17	US-10-104-047-669	Sequence 669, App
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ALIGNMENTS

RESULT 1
US-09-918-715-176
; Sequence 176, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0

OM protein - protein search, using sw model

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            GenCore version 5.1.6
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Post:processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	199	6.6	104	4	US-09-547-693-235	Sequence 235, App
2	199	6.6	288	4	US-09-270-767-42632	Sequence 42632, A
3	195	6.4	498	4	US-09-949-016-7108	Sequence 7108, Ap
4	191.5	6.3	306	1	US-08-217-327-6	Sequence 6, Appli
5	186	6.1	76	4	US-09-547-693-233	Sequence 233, App
6	186	6.1	214	1	US-08-217-327-4	Sequence 4, Appli
7	178.5	5.9	802	4	US-09-823-240A-2	Sequence 2, Appli
8	175	5.8	294	4	US-09-270-767-36084	Sequence 36084, A
9	175	5.8	294	4	US-09-270-767-51301	Sequence 51301, A
10	173.5	5.7	142	4	US-09-252-991A-24873	Sequence 24873, A
11	173.5	5.7	334	6	5202236-3	Patent No. 5202236
12	173.5	5.7	334	6	5202236-3	Patent No. 5202236
13	173.5	5.7	971	4	US-09-248-796A-19531	Sequence 19531, A
14	172	5.7	553	4	US-09-949-016-7961	Sequence 7961, Ap
15	171.5	5.7	331	6	5202236-37	Patent No. 5202236
16	171.5	5.7	331	6	5202236-37	Patent No. 5202236
17	170	5.6	581	4	US-09-949-016-9978	Sequence 9978, Ap
18	167.5	5.5	1248	2	US-09-080-897-2	Sequence 2, Appli
19	167.5	5.5	1248	3	US-09-323-735-2	Sequence 2, Appli
20	167	5.5	1231	4	US-08-714-741-41	Sequence 41, Appl
21	166	5.5	1155	1	US-08-286-889-46	Sequence 46, Appl
22	166	5.5	1155	1	US-08-485-618-46	Sequence 46, Appl
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25	166	5.5	1155	2	US-08-482-293A-46	Sequence 46, Appl
26	166	5.5	1155	2	US-08-943-363-46	Sequence 46, Appl
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32	166	5.5	1161	2	US-08-605-672-53	Sequence 53, Appl
33	166	5.5	1161	2	US-08-482-293A-53	Sequence 53, Appl
34	166	5.5	1161	3	US-08-943-363-53	Sequence 53, Appl
35	166	5.5	1161	3	US-09-193-043-53	Sequence 53, Appl
36	166	5.5	1161	4	US-09-688-307A-53	Sequence 53, Appl
37	166	5.5	1161	4	US-09-350-259-53	Sequence 53, Appl
38	165	5.5	105	4	US-09-547-693-230	Sequence 230, App
39	164	5.4	511	4	US-09-107-433-2904	Sequence 2904, Ap
40	163	5.4	635	4	US-07-832-855-2	Sequence 2, Appli
41	162.5	5.4	203	4	US-09-543-681A-8287	Sequence 8287, Ap
42	162	5.4	559	4	US-10-116-370-2	Sequence 2, Appli
43	162	5.4	567	4	US-09-949-016-10952	Sequence 10952, A
44	161.5	5.3	506	4	US-09-949-016-11282	Sequence 11282, A
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ALIGNMENTS

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; Sequence 235, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic
US-09-547-693-235

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Qy    543 PPQAPPNRAPPPSRPPPRP 562
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; Sequence 42632, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42632
; LENGTH: 288
; TYPE: PRT

OM protein - protein search, using sw model

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                    GenCore version 5.1.6
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Perfect score: 3025

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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4	3025	100.0	564	16	564	US-10-408-765A-1823	Sequence 1823, Ap
5	2901	95.9	562	10	562	US-09-918-715-194	Sequence 194, App
6	2901	95.9	562	10	562	US-09-918-715-301	Sequence 301, App
7	2017	66.7	381	10	381	US-09-796-753-24	Sequence 24, Appl
8	2017	66.7	381	14	381	US-10-038-307-4	Sequence 4, Appli
9	2017	66.7	381	14	381	US-10-201-292-4	Sequence 4, Appli
10	1893.5	62.6	403	11	403	US-09-833-245-621	Sequence 621, App
11	1874	62.0	403	11	403	US-09-833-245-620	Sequence 620, App
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13	1661	54.9	551	14	551	US-10-201-292-18	Sequence 18, Appl
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15	1649	54.5	333	14		US-10-038-307-2	Sequence 2, Appli
16	1649	54.5	333	14		US-10-201-292-2	Sequence 2, Appl
17	1649	54.5	345	14		US-10-038-307-24	Sequence 24, Appl
18	1649	54.5	345	14		US-10-201-292-24	Sequence 24, Appl
19	1649	54.5	564	14		US-10-038-307-20	Sequence 20, Appl
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21	1636	54.1	328	14		US-10-038-307-26	Sequence 26, Appl
22	1636	54.1	328	14		US-10-201-292-26	Sequence 26, Appl
23	1634.5	54.0	342	14		US-10-038-307-22	Sequence 22, Appl
24	1634.5	54.0	342	14		US-10-201-292-22	Sequence 22, Appl
25	1629	53.9	543	14		US-10-038-307-14	Sequence 14, Appl
26	1629	53.9	543	14		US-10-038-307-16	Sequence 16, Appl
27	1629	53.9	543	14		US-10-201-292-14	Sequence 14, Appl
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31	1552.5	51.3	529	14		US-10-201-292-36	Sequence 36, Appl
32	1488	49.2	534	14		US-10-038-307-12	Sequence 12, Appl
33	1488	49.2	534	14		US-10-201-292-12	Sequence 12, Appl
34	1434.5	47.4	504	14		US-10-201-292-34	Sequence 34, Appl
35	1416.5	46.8	488	14		US-10-368-087-16	Sequence 16, Appl
36	1416.5	46.8	488	15		US-10-104-047-2639	Sequence 2639, Ap
37	1411.5	46.7	488	10		US-09-796-753-52	Sequence 52, Appl
38	1411.5	46.7	488	14		US-10-038-307-6	Sequence 6, Appli
39	1411.5	46.7	488	14		US-10-201-292-6	Sequence 6, Appl
40	1396.5	46.2	487	10		US-09-796-753-54	Sequence 54, Appl
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42	1396.5	46.2	487	14		US-10-201-292-8	Sequence 8, Appli
43	1396.5	46.2	487	14		US-10-368-087-15	Sequence 15, Appl
44	1307	43.2	479	14		US-10-201-292-32	Sequence 32, Appl
45	1206.5	39.9	587	9		US-09-764-870-312	Sequence 312, App

ALIGNMENTS

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; Sequence 187, Application US/09918715
; Publication No. US2003017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
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           GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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5	166	8.7	3519	1	US-08-485-618-45	Sequence 45, Appl
6	166	8.7	3519	1	US-08-362-652-45	Sequence 45, Appl
7	166	8.7	3519	2	US-08-605-672-45	Sequence 45, Appl
8	166	8.7	3519	2	US-08-482-293A-45	Sequence 45, Appl
9	166	8.7	3519	3	US-08-943-363-45	Sequence 45, Appl
10	166	8.7	3519	3	US-09-193-043-45	Sequence 45, Appl
11	166	8.7	3519	3	US-09-688-307A-45	Sequence 45, Appl
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19	166	8.7	3803	3	US-09-688-307A-52	Sequence 52, Appl
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; GENERAL INFORMATION:
;  APPLICANT: Tang, Y., Tom
;  APPLICANT: Liu, Chenghua
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Zhang, Jie
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Chen, Rui-hong
;  APPLICANT: Zhao, Qing A.
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: Yang, Yonghong
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Zhou, Ping
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Wang, Zhiwei
;  APPLICANT: John Tillinghast
;  APPLICANT: Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 656962el Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312D
;  CURRENT FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 1105
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 8
;  LENGTH: 1609
;  TYPE: DNA
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            Copyright   GenCore version 5.1.6
                        Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score:  1914
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	166	8.7	1155	1	US-08-286-889-46	Sequence 46, Appl
2	166	8.7	1155	1	US-08-485-618-46	Sequence 46, Appl
3	166	8.7	1155	1	US-08-362-652-46	Sequence 46, Appl
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5	166	8.7	1155	2	US-08-482-293A-46	Sequence 46, Appl
6	166	8.7	1155	2	US-08-943-363-46	Sequence 46, Appl
7	166	8.7	1155	4	US-09-193-043-46	Sequence 46, Appl
8	166	8.7	1155	4	US-09-688-307A-46	Sequence 46, Appl
9	166	8.7	1155	4	US-09-350-259-46	Sequence 46, Appl
10	166	8.7	1161	1	US-08-485-618-53	Sequence 53, Appl
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18	159.5	8.3	1151	1	US-08-286-889-37	Sequence 37, Appl
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23	159.5	8.3	1151	2	US-08-943-363-37	Sequence 37, Appl
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25	159.5	8.3	1151	4	US-09-688-307A-37	Sequence 37, Appl
26	159.5	8.3	1151	4	US-09-350-259-37	Sequence 37, Appl
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28	159.5	8.3	1161	1	US-08-286-889-2	Sequence 2, Appli
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ALIGNMENTS

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RESULT 1
US-08-286-889-46

; Sequence 46, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
;   APPLICANT: Gallatin, W. Mich.
;   APPLICANT: Van der Vieren, Monica
;   TITLE OF INVENTION: No. 5470953el Human  2 Integrin Alpha Subunit
;   NUMBER OF SEQUENCES: 51
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 233 South Wacker Drive, 6300 Sear Tower
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: United States
;   ZIP: 60606-6402
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/286,889
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/173,497
;   FILING DATE: 23-DEC-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Williams Jr., Joseph A.
;   REGISTRATION NUMBER: P38,659
;   REFERENCE/DOCKET NUMBER: 27866/32168
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-474-6300
;   TELEFAX: 312-474-0448
;   TELEX: 25-3856
;   INFORMATION FOR SEQ ID NO: 46:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1155 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-286-889-46

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Matches  66;  Conservative  42;  Mismatches  96;  Indels  30;  Gaps  12;

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OM protein - protein search, using sw model

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score:  1914
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Total number of hits satisfying chosen parameters:        1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1894	99.0	564	10	US-09-918-715-187	Sequence 187, App
2	1894	99.0	564	10	US-09-918-715-232	Sequence 232, App
3	1894	99.0	564	14	US-10-301-822-199	Sequence 199, App
4	1894	99.0	564	16	US-10-408-765A-1823	Sequence 1823, Ap
5	1889	98.7	403	11	US-09-833-245-621	Sequence 621, App
6	1870	97.7	403	11	US-09-833-245-620	Sequence 620, App
7	1793	93.7	562	10	US-09-918-715-194	Sequence 194, App
8	1793	93.7	562	10	US-09-918-715-301	Sequence 301, App
9	1661	86.8	551	14	US-10-038-307-18	Sequence 18, Appl
10	1661	86.8	551	14	US-10-201-292-18	Sequence 18, Appl
11	1649	86.2	333	10	US-09-796-753-12	Sequence 2, Appl
12	1649	86.2	333	14	US-10-038-307-2	Sequence 2, Appli
13	1649	86.2	333	14	US-10-201-292-2	Sequence 2, Appli
14	1649	86.2	345	14	US-10-038-307-24	Sequence 24, Appl
15	1649	86.2	345	14	US-10-201-292-24	Sequence 24, Appl
16	1649	86.2	564	14	US-10-038-307-20	Sequence 20, Appl
17	1649	86.2	564	14	US-10-201-292-20	Sequence 20, Appl
18	1636	85.5	328	14	US-10-038-307-26	Sequence 26, Appl
19	1636	85.5	328	14	US-10-201-292-26	Sequence 26, Appl
20	1634.5	85.4	342	14	US-10-038-307-22	Sequence 22, Appl
21	1634.5	85.4	342	14	US-10-201-292-22	Sequence 22, Appl
22	1629	85.1	543	14	US-10-038-307-14	Sequence 14, Appl
23	1629	85.1	543	14	US-10-038-307-16	Sequence 16, Appl
24	1629	85.1	543	14	US-10-201-292-14	Sequence 14, Appl
25	1629	85.1	543	14	US-10-201-292-16	Sequence 16, Appl
26	1619	84.6	543	14	US-10-038-307-10	Sequence 10, Appl
27	1619	84.6	543	14	US-10-201-292-10	Sequence 10, Appl
28	1548	80.9	529	14	US-10-201-292-36	Sequence 36, Appl
29	1488	77.7	534	14	US-10-038-307-12	Sequence 12, Appl
30	1488	77.7	534	14	US-10-201-292-12	Sequence 12, Appl
31	1434.5	74.9	504	14	US-10-201-292-34	Sequence 34, Appl
32	1307	68.3	479	14	US-10-201-292-32	Sequence 32, Appl
33	1193	62.3	460	14	US-10-201-292-28	Sequence 28, Appl
34	1183	61.8	460	14	US-10-201-292-30	Sequence 30, Appl
35	962.5	50.3	488	14	US-10-368-087-16	Sequence 16, Appl
36	962.5	50.3	488	15	US-10-104-047-2639	Sequence 2639, Ap
37	957.5	50.0	488	10	US-09-796-753-52	Sequence 52, Appl
38	957.5	50.0	488	14	US-10-038-307-6	Sequence 6, Appli
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42	938.5	49.0	587	14	US-10-125-540-312	Sequence 312, App
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44	936.5	48.9	487	14	US-10-038-307-8	Sequence 8, Appli
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ALIGNMENTS

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; Sequence 187, Application US/09918715
; Publication No. US2003001715TA1
; GENERAL INFORMATION:
;  APPLICANT: Brad St. Croix
;  APPLICANT: Bert Vogelstein
;  APPLICANT: Kenneth Kinzler
;  TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;  FILE REFERENCE: 1107.00134
;  CURRENT APPLICATION NUMBER: US/09/918,715
;  CURRENT FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/222,599
;  PRIOR FILING DATE: 2000-08-02
;  PRIOR APPLICATION NUMBER: 60/224,360
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: 60/282,850
;  PRIOR FILING DATE: 2000-04-11
;  NUMBER OF SEQ ID NOS: 358
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187

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  Matches  364;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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